



SEQUENCE LISTING

<110> KATO, Seishi
KIMURA, Tomoko

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 2003-0984/WMC/01791

<140> 10/019,151

<151> 2002-08-20

<150> PCT/JP00/03944

<151> 2000-06-16

<150> JP 11-178065

<151> 1999-06-24

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Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val
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Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly
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Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile
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Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe
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Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu
145 150 155 160
Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val
165 170 175
Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile
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Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala
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Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
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Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
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Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
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Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
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Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
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Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
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Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
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 225 230 235 240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
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Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
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 Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
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 35 40 45
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 Arg Ser Phe Ile Glu Leu Thr Pro Ala Lys Arg Glu Ile Leu Trp
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 130 135 140
 Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn Pro Ala Cys
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 Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val Leu Ser Gly
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 Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys Cys Met Ala
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Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val Leu Glu Phe
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 245 250 255
 His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala Ala Pro Thr
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 Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln Pro Ile His
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 Pro Ala Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr
 65 70 75 80
 Asn Lys Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala
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 Phe Val Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys
 100 105 110
 Thr Phe Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr
 115 120 125
 Val Leu Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser
 130 135 140
 Val Leu Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr
 145 150 155 160
 Tyr Val Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg
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 Glu Gly Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu
 180 185 190
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 35 40 45
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 His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65 70 75 80
 Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr
 85 90 95
 Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu
 100 105 110
 Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr
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 50 55 60
 His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65 70 75 80
 Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr
 85 90 95
 Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu
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 Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr
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 35 40 45
 Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg
 50 55 60
 Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu
 65 70 75 80
 Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val
 85 90 95
 Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe
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 Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser
 115 120 125

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 145 150 155 160
 Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met
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 Leu Glu Lys Thr Ile His Glu Glu
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 35 40 45
 Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
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 Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
 65 70 75 80
 Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser
 85 90 95
 Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
 100 105 110
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 115 120 125
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aaccatgaat ttgtacactg tgccccagaa atcgaaaagt tattccagtc ggtcgcacag 660
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ttcctgttca gacgctgctt caagggttaa catgatgctt tgaagacata tgcattcattg 240
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tatagtgtat atagtttttag aaaaacagtc ccaccactta agcatagatg taattttacta 180
ataaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228
Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val
1 5 10
gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276
Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe
15 20 25 30
act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324
Thr Gly Val Met Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu
35 40 45
aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372
Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu
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Gln Val Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn
65 70 75
gca ctg gtg ctc tat gtc ggg act cag gcc att gcg cac atc cac aac 468
Ala Leu Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn
80 85 90
aag ggc agc aca cct tca atg agc acc atc act cac tca gca cac atg 516
Lys Gly Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met
10

95	gat atc ttc cag aat ttg gct gtg gac ttg gac act gag ggt cgc tat	100	105	110	564
Asp Ile Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr					
ctc ttt ttg aat gca att gca aat cag ctc cgg tac cca aat agc cac	115	120	125	612	
Leu Phe Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His					
act cac tac ttc agt tgc acc atg ctg tac ctt ttt gca gag gcc aat	130	135	140	660	
Thr His Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn					
acg gaa gcc atc caa gaa cag atc aca aga gtt ctc ttg gaa cgg ttg	145	150	155	708	
Thr Glu Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu					
att gta aat agg cca cat cct tgg ggt ctt ctt att acc ttc att gag	160	165	170	756	
Ile Val Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu					
ctg att aaa aac cca gcg ttt aag ttc tgg aac cat gaa ttt gta cac	175	180	185	804	
Leu Ile Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His					
tgt gcc cca gaa atc gaa aag tta ttc cag tcg gtc gca cag tgc tgc	190	195	200	852	
Cys Ala Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys					
atg gga cag aag cag gcc cag caa gta atg gaa ggg aca ggt gcc agt	205	210	215	900	
Met Gly Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser					
tagacgaaac tgcattctctg ttgtacgtgt cagtctagag gtctcactgc accgagttca	225	230	235	960	
taaactgact gaagaatcct ttcagctctt cctgactttc ccagcccctt ggtttgtggg				1020	
tatctgcccc aactactgtt gggatcagcc tcctgtctta tgtgggcacg ttccaaagtt				1080	
taaattgcatt tttttgactc ttggccaaaaa tttagaagat gctgtgaata tcattttgaa				1140	
cttgtgtgaaa tacatgaaag agaaaaac				1167	

<210> 18
 <211> 1925
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (115)... (1134)

<400> 18	gttccttcgc cgccgccagg ggtagcggtg tagctgcgca gcgtcgcgcg cgctaccgca	60
cccaggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg		117
	Met	1
gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc		165
Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly		
ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac	5	10
Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp		15
cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat	20	25
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr		30
gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa	35	40
Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys		45
tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata	50	55
Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile		60
cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt	65	70
Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys		75
	80	85
	90	95

aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc	453
Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser	
100 105 110	
tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct	501
Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser	
115 120 125	
tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa	549
Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys	
130 135 140 145	
ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat	597
Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr	
150 155 160	
tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att	645
Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile	
165 170 175	
acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc	693
Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe	
180 185 190	
ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca	741
Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro	
195 200 205	
ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc	789
Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro	
210 215 220 225	
cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggr cat ggt	837
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly	
230 235 240	
gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa	885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu	
245 250 255	
aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta	933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu	
260 265 270	
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg	981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser	
275 280 285	
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg	1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg	
290 295 300 305	
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca	1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser	
310 315 320	
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg	1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg	
325 330 335	
aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggatttt	1180
Arg Arg	
tcatcacttt ctcttttagaa aaaaagtact acctgttaac aattgggaaa aggggatatt	1240
caaaagttct gtgggtgttat gtccagtgtg gctttttgta ttctattatt tgaggctaaa	1300
agttgatgtg tgacaaaata cttatgtggt gtatgtcagt gtaacatgca gatgtatatt	1360
gcagtttttg aaagtgatca ttactgtgga atgctaaaaa tacattaatt tctaaaacct	1420
gtgatgccct aagaagcatt aagaatgaag gtgttgact aatagaaact aagtacagaa	1480
aatttcagtt ttagggtggt gtagctgatg agttattacc tcatagagac tataatatcc	1540
tatttggtat tatattatct gatgtttgct gttcttcaaa catttaaact aagctttgga	1600
ctaattatgc taatttgtga gttctgatca cttttgagct ctgaagcttt gaatcattca	1660
gtggtggaga tggccttctg gtaactgaat attaccttct gtaggaaaag gtggaaaata	1720
agcatctaga aggttggtgt gaatgactct gtgctggcaa aatgcttga aacctctata	1780
tttctttcgt tcataagagg taaaggctaa atttttcaac aaaagtcttt taataacaaa	1840
agcatgcagt tctctgtgaa atctcaaata ttgttgtaat agtctgtttc aatcttaaaa	1900
agaatcaata aaaacaaaca agggg	1925

<211> 1125
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (71) ... (1051)

<400> 19
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 gacgctgacc atg gcc aag atg gag ctc tcg aag gcc ttc tct ggc cag 109
 1 5 10
 cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157
 Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser
 15 20 25
 aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205
 Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val
 30 35 40 45
 ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg 253
 Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met
 50 55
 cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag gtg gta 301
 Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val
 65 70 75
 caa tac aac tgg gag act ggg gat gac cgg ttc tcc ttc cgg agc ttc 349
 Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe
 80 85 90
 cgg agt ggc atg tgg cta tcc tgt gag gaa act gtg gaa gaa cca ggg 397
 Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly
 95 100 105
 gag agg tgc cga agt ttc att gaa ctt aca cca cca gcc aag aga gaa 445
 Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu
 110 115 120 125
 atc cta tgg tta tcc ctg gga acg cag atc acc tac atc gga ctt caa 493
 Ile Leu Trp Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln
 130 135
 ttc atc agc ttc ctc ctg cta cta aca gac ttg cta ctc act ggg aac 541
 Phe Ile Ser Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn
 145 150 155
 cct gcc tgt ggg ctc aaa ctg agc gcc ttt gct gct gtt tcc tct gtc 589
 Pro Ala Cys Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val
 160 165 170
 ctg tca ggt ctc ctg ggg atg gtg gcc cac atg atg tat tca caa gtc 637
 Leu Ser Gly Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val
 175 180 185
 ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt 685
 Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val
 190 195 200 205
 tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc 733
 Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys
 210 215 220
 tgc atg gcg tgc gct gtc acc acc ttc aac acg tac acc agg atg gtg 781
 Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val
 225 230 235
 ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac 829
 Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn
 240 245 250
 tgc cta cca cat cac cat cag tgt ttc cct cgg cgg ctg tca agt gca 877
 Cys Leu Pro His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala
 255 260 265
 gcc ccc acc gtg ggt cct ttg acc agc tac cac cag tat cat aat cag 925
 Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln
 270 275 280 285

ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg	973
Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg	
290 295 300	
aac aag gga ttt caa aga ggg gcc agc cag gag ctg aaa gaa gca gtt	1021
Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val	
305 310 315	
agg tca tct gta gag gaa gag cag tgt taggagttaa gcggggtttgg gg	1070
Arg Ser Ser Val Glu Glu Glu Gln Cys	
320 325	
agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc	1125

<210> 20
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (40) ... (1014)

<400> 20	
ctcttgcggc gcccggtgcgc ggccggcccg gcaggcgagg atg gcg gcc gcg gct	54
Met Ala Ala Ala Ala	
1 5	
ccg gag aac ggc cgc gca tcg gcg ccc cgg ctg ctt ctg ctc ttt ctg	102
Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Leu Phe Leu	
10 15 20	
gtt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa	150
Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu	
25 30 35	
gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccg gcc cag cag ctg	198
Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu	
40 45 50	
cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag	246
Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu	
55 60 65	
aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat cct	294
Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro	
70 75 80 85	
gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata	342
Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile	
90 95 100	
tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca	390
Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala	
105 110 115	
gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca	438
Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala	
120 125 130	
atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat	486
Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr	
135 140 145	
gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta	534
Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val	
150 155 160 165	
tta ttt gcc att ttt ggc att aga atg ctt cgg gaa ggc tta aag atg	582
Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met	
170 175 180	
agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta	630
Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu	
185 190 195	
aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg	678
Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Asn Gly Pro	
200 205 210	

gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg	726
Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp	
215 220 225	
ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc	774
Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe	
230 235 240 245	
tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca	822
Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala	
250 255 260	
gct aga gag gac ccc tat ggt gta gcc gtg ggt gga act gtg ggg cac	870
Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His	
265 270 275	
tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag	918
Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln	
280 285 290	
aaa atc tct gtc aga act gtg aca atc ata aga ggc atc gtt ttt ttg	966
Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu	
295 300 305	
gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt	1011
Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe	
310 315 320	
taacgctgt ttgttcatct atatttagtt taaaataggt agtattatct ttctgtacat	1070
agtgtacatt acaactaaaa gtgatggaaa aatactgtat tttgtagcac tgattttgtg	1130
agtttgaccc attattatgt ctgagatata atcattgatt ctatttgtaa caaggagttt	1190
taaaagaaac ctgacttcta agtgtgggtt tttcttctct ccaacataat tatgttaata	1250
tggtcctcat ttttcttttg gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt	1310
ctttcagcac tgacccttt ttaaggaata caaattttct ccttcacac ttaggtgttt	1370
taagatgttt accttaaagt ttttcttggg gaaagaatga attaatttct atttcttaaa	1430
acatttccct gagccagtaa acagtagttt aatcattggt cttttcaaaa ctagggtgttt	1490
aaaaaaagag acatatatga tattgctgtt atatcaataa catggcacia caagaactgt	1550
ctgccagggtc attcttccctc tttttttttt aattgggtag gacacccaat ataaaaacag	1610
tcaatatttg acaatgtgga attaccaa ataaaagagaa tactatgaat gtattcatat	1670
tttttctata ttgaataaac aatgtaacat agataacaat ataaataaaa gtggtatgac	1730
cagt	1734

<210> 21
 <211> 2064
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (98) ... (559)

<400> 21	
aaaacagctg ctggagcagc agcggccccc gtcctcgga accgttcccg ggccgttgat	60
cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca	112
Met Asn Val Gly Thr	
1 5	
gcg cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc	160
Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly	
10 15 20	
atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg	208
Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu	
25 30 35	
ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac	256
Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn	
40 45 50	
ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg	304
Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly	
55 60 65	
aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac	352
Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His	
15	

70	75	80	85	
tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc				400
Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe				
	90	95	100	
ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act				448
Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr				
	105	110	115	
aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc				496
Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser				
	120	125	130	
gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga				544
Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly				
	135	140	145	
atc aat aag tac tgagagtga gccccttccc ctgccagggtg tggcagggga gggg				600
Ile Asn Lys Tyr				
150				
tagggtaaaa ggcattgtgct gcaacactga agacagaaaag aagaagcctc tggacactgc				660
cagagatggg ggttgagcct ctggcctaata tccccccctc gcttccccca gtagccaaact				720
tggagtagct tgtagtgggg ttggggtagg ccccttgggc tctgaccttt tctgaatttt				780
ttgatctttt ccttttgctt tttgaataga gactccatgg agtttgtcat ggaatgggct				840
gggctcctgg gctgaacatg gaccacgcag ttgcgacagg aggccagggg aaaaaccctt				900
gctcacttgt ttgccctcag gcagccaaag cactttaacc cctgcatagg gagcagaggg				960
cggtagcggct tctggattgt ttcactgtga ttcctagggt ttttcgatgc cacgcagtgt				1020
gtgcttttgt gtatggaagc aagtgtggga tgggtctttg ctttctggg tagggagctg				1080
tctaatacaa gtcccaggct tttggcagct tctctgcaac ccaccgtggg tcctggttgg				1140
gagtggggag ggtcaggttg gggaaagatg gggtagagtg tagatggctt ggttccagag				1200
gtgagggggc cagggctgct gccatccttg cctggtggag gttggggagc tgtaggagag				1260
ctagtgaagc gagacttaga agaattggggc cacatagcag cagaggactg gtgtaaggga				1320
gggaggggta gggacagaag ctagacccaa tctcctttgg gatgtgggca gggaggggaag				1380
caggcttgga ggggttaattt acccacagaa tgtgatagta ataggggagg gaggctgctg				1440
tgggtttaac tcctgggttg gctgttggtt agacaggttg ggaaaaggcc cgtgagtcac				1500
tgtaaacaca ggtccaactt ggccctgact cctgcggggg tatggggaag ctgtgacaga				1560
aacgatgggt gctgtggtcc tctgcaggcc ctcacccctt aacttctca tacagactgg				1620
caactgggag ggcctctcat gtggcagcca catgtggcgt tgtgaggcca ccccatgttg				1680
ggtctgtggt gagagtcctg taggatccct gctcaaggcag cacagaggaa ggggcaagac				1740
gtggcctgta ggcactgttt cagcctgcag agaagaaagt gaggccggga gcctgagcct				1800
gggctggagc cttctcccct ccccagtttg actaggggca gtgttaattt tgaaaagggtg				1860
tgggtccctg tgtcctcttc caggggtcca agggaacagg agaggctact gggcctgttt				1920
tctccctcct gacctgcat ctcccacccc gtgtatcata gggaactttc accttaaaat				1980
ctttctaagc aaagtgtgaa taggattttt actccctttg tacagtattc tgagaaacgc				2040
aaataaaaagg gcaacatgtt tctg				2064

<210> 22
 <211> 570
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (28) ... (489)

<400> 22	
agccggacgg ggaatctgagc tggcagg atg aat gtg ggg gtg gca cac agc	51
Met Asn Val Gly Val Ala His Ser	
gaa gta aac ccc aac acc cga gtg atg aat agc cga ggc atc tgg ctg	99
Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu	
gcc tac atc atc ttg gta gga ttg ctg cat atg gtt cta ctc agc atc	147
Ala Tyr Ile Ile Leu Val Gly Leu Leu His Met Val Leu Leu Ser Ile	
ccc ttc ttc agc att cct gtt gtc tgg acc acc aac gtc atc cat	195
Pro Phe Phe Ser Ile Pro Val Val Trp Thr Leu Thr Asn Val Ile His	

aac	ctg	gct	acg	tat	gtc	ttc	ctt	cat	acg	gtg	aaa	ggg	aca	ccc	ttt	243
Asn	Leu	Ala	Thr	Tyr	Val	Phe	Leu	His	Thr	Val	Lys	Gly	Thr	Pro	Phe	
			60					65					70			
gag	act	cct	gac	caa	gga	aag	gct	cgg	cta	ctg	aca	cac	tgg	gag	caa	291
Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala	Arg	Leu	Leu	Thr	His	Trp	Glu	Gln	
		75					80					85				
atg	gac	tat	ggg	ctc	cag	ttt	acc	tct	tcc	cgc	aag	ttc	ctc	agc	atc	339
Met	Asp	Tyr	Gly	Leu	Gln	Phe	Thr	Ser	Ser	Arg	Lys	Phe	Leu	Ser	Ile	
		90				95					100					
tct	cct	att	gtg	ctc	tat	ctc	ctg	gcc	agc	ttc	tat	acc	aag	tat	gat	387
Ser	Pro	Ile	Val	Leu	Tyr	Leu	Leu	Ala	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp	
					110					115					120	
gct	gcg	cac	ttc	ctc	atc	aac	aca	gcc	tca	ttg	cta	agt	gta	ctg	ctg	435
Ala	Ala	His	Phe	Leu	Ile	Asn	Thr	Ala	Ser	Leu	Leu	Ser	Val	Leu	Leu	
			125						130					135		
ccg	aag	ttg	ccc	cag	ttc	cat	ggg	gtt	cgt	gtc	ttt	ggc	atc	aac	aaa	483
Pro	Lys	Leu	Pro	Gln	Phe	His	Gly	Val	Arg	Val	Phe	Gly	Ile	Asn	Lys	
			140				145					150				
tac	tgag	ggatggg	ttt	tg	ggacag	ct	ccatggg	cat	ggggaagg	ca	ctgaaacaga					540
Tyr																
ggactataaa	acatccttct	cttattctcc														570

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (278)... (880)

<400> 23																
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ggtgtggtgc	cggtgggaac	tgaggaagcg	cccaaggaaa	tgaaacacga	tttccaaaat											120
gaacttaatc	tttcatgaga	aactgaggat	agagatgtca	ataagcagcc	actgtttcca											180
cctccccacc	tgaagagcta	ggaggacaac	tacaaagagc	ctgactgcct	tctcggaatg											240
aggagagagg	aaaacagcaa	cagtatcagt	tttcaag	atg	gca	gca	tct	atg								292
				Met	Ala	Ala	Ser	Met								
				1				5								
cat	ggt	cag	ccc	agt	cct	tct	cta	gaa	gat	gca	aaa	ctc	aga	aga	cca	340
His	Gly	Gln	Pro	Ser	Pro	Ser	Leu	Glu	Asp	Ala	Lys	Leu	Arg	Arg	Pro	
				10					15					20		
atg	gtc	ata	gaa	atc	ata	gaa	aaa	aat	ttt	gac	tat	ctt	aga	aaa	gaa	388
Met	Val	Ile	Glu	Ile	Ile	Glu	Lys	Asn	Phe	Asp	Tyr	Leu	Arg	Lys	Glu	
		25						30					35			
atg	aca	caa	aat	ata	tat	caa	atg	gcg	aca	ttt	gga	aca	aca	gct	ggt	436
Met	Thr	Gln	Asn	Ile	Tyr	Gln	Met	Ala	Thr	Phe	Gly	Thr	Thr	Ala	Gly	
		40					45					50				
ttc	tct	gga	ata	ttc	tca	aac	ttc	ctg	ttc	aga	cgc	tgc	ttc	aag	gtt	484
Phe	Ser	Gly	Ile	Phe	Ser	Asn	Phe	Leu	Phe	Arg	Arg	Cys	Phe	Lys	Val	
		55				60					65					
aaa	cat	gat	gct	ttg	aag	aca	tat	gca	tca	ttg	gct	aca	ctt	cca	ttt	532
Lys	His	Asp	Ala	Leu	Lys	Thr	Tyr	Ala	Ser	Leu	Ala	Thr	Leu	Pro	Phe	
		70			75					80					85	
ttg	tct	act	gtt	gtt	act	gac	aag	ctt	ttt	gta	att	gat	gct	ttg	tat	580
Leu	Ser	Thr	Val	Val	Thr	Asp	Lys	Leu	Phe	Val	Ile	Asp	Ala	Leu	Tyr	
			90						95					100		
tca	gat	aat	ata	agc	aag	gaa	aac	tgt	gtt	ttc	aga	agc	tca	ctg	att	628
Ser	Asp	Asn	Ile	Ser	Lys	Glu	Asn	Cys	Val	Phe	Arg	Ser	Ser	Leu	Ile	
			105					110					115			
ggc	ata	gtt	tgt	ggt	gtt	ttc	tat	ccc	agt	tct	ttg	gct	ttt	act	aaa	676
										17						

Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys	
120 125 130	
aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa	724
Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys	
135 140 145	
gga agg gtt tta atc cat tgg atg acg ctt tgt caa aca caa atg aaa	772
Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys	
150 155 160 165	
tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat	820
Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn	
170 175 180	
ggt cta tac cat tat gca gta ttt gaa gag aca ctt gag aaa act ata	868
Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile	
185 190 195	
cat gaa gag taacacaaaaa aatgaatggt tgctaactta gcaaaatgaa gtt	920
His Glu Glu	
200	
tctataaaga ggactcaggc attgctgaaa gagttaaaag taactgtgaa caaataattt	980
gttctgtgcc ttttgcctgg tatatagcaa atactcaaaa agtattcaat aattcaatca	1040
ataaatataa gtttcatctt acacgtaaga tacagggtctt atctcctgat ggtgtgtcca	1100
ttttgcctgg tatataacag ataataaata tccagtgtca ataaatgtaa caataaaagt	1160
t	1161

<210> 24
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (58) ... (627)

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Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala	
1 5 10 15	
atc cca ggg ggc ctc ggg gac agg gcg cca ctc aca gcc aca gcc cca	153
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro	
20 25 30	
caa ctg gat gat gag gag atg tac tca gcc cac atg ccc gct cac ctg	201
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu	
35 40 45	
cgc tgt gat gcc tgc aga gct gtg gct tac cag atg tgg caa aat ctg	249
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu	
50 55 60	
gca aag gca gag acc aaa ctt cat acc tca aac tct ggg ggg cgg cgg	297
Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg	
65 70 75 80	
gag ctg agc gag ttg gtc tac acg gat gtc ctg gac cgg agc tgc tcc	345
Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser	
85 90 95	
cgg aac tgg cag gac tac gga gtt cga gaa gtg gac caa gtg aaa cgt	393
Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg	
100 105 110	
ctc aca ggc cca gga ctt agc gag ggg cca gag cca agc atc agc gtg	441
Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val	
115 120 125	
atg gtc aca ggg ggc ccc tgg cct acc agg ctc tcc agg aca tgt ttg	489
Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu	
130 135 140	
cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa	537
His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln	
145 150 155 160 165 170 175 180 185 190 195 200	

145		150		155		160	
caa ggc cga ggg gct ctg gag gca ttg cta tgt ggg gga ccc cag ggg	585						
Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly							
165	170	175					
gcc tgc tca gag aag gtg tca gcc aca aga gaa gag ctc tagtcc	630						
Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu							
180	185						
tggaactctac cctcctctga aagaagctgg ggcttgctct gacgggtctcc actcccgtct	690						
gcaggcagcc aggagggcag gaagcccttg ctctgtgctg ccatacctgcc tccctcctcc	750						
agcctcaggg cactcgggcc tgggtgggag tcaacgcctt cccctctgga ctcaaataaa	810						
acccagtgc ctc	823						